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RAW SEQUENCE LISTING

DATE: 09/26/2001

PATENT APPLICATION: US/09/943,108

TIME: 12:19:40

Input Set : N:\Crif3\RULE60\09943108.txt

Output Set: N:\CRF3\09262001\I943108.raw

4 <110> APPLICANT: Black, Michael T.
 7 <120> TITLE OF INVENTION: SIGNAL RECOGNITION PARTICLE POLYPEPTIDES
 8 AND POLYNUCLEOTIDES
 10 <130> FILE REFERENCE: GM50035
 12 <140> CURRENT APPLICATION NUMBER: 09/943,108
 C--> 13 <141> CURRENT FILING DATE: 2001-08-30
 15 <150> PRIOR APPLICATION NUMBER: 09/035,382
 16 <151> PRIOR FILING DATE: 1998-05-03
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1368
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Staphylococcus aureus
 27 <400> SEQUENCE: 1
 28 atggcatttg aaggcttatc agaacgcctg caagcgacga tgcaaaaaat gcgtggtaag 60
 29 ggtaaactta ctgaagctga tataaagata atgatgcgtg aagtaagatt agcgttattt 120
 30 gaggctgacg taaactttaa agtggtaaaa gaatttatta aaacagtatc agaacgcgca 180
 31 ttaggttccg atgtaatgca atcattaaca ccagggcaac aagttattaa aatagttcaa 240
 32 gatgaattaa cgaagttgat ggggtggagaa aatacatcga ttaatatgtc aaataaacca 300
 33 cctactgttg ttatgatggg tggtttaca ggtgctggta aaacaacaac tgcaggtaaa 360
 34 tttagcattat tgaatgcgtaa aaaatacaac aaaaaaccta tgtagttgac agcagatatt 420
 35 tatcgctccag cagcgataaa tcaattacaa acagtaggga aacaaattga tattcctgta 480
 36 tacagtgaag gagatcaagt aaagccacaa caaattgtaa ctaatgcatt aaaacatgct 540
 37 aaagaagaac atttagactt tgtaatcatt gatacagcag gtcgattaca catcgatgaa 600
 38 gcattgatga acgaattaaa agaagtaaaa gaaattgcta aaccaaacga aattatgtta 660
 39 gttgtcgatt caatgacggg tcaagatgct gtcaatgttg cagaatcttt tgacgatcaa 720
 40 cttgatgtca caggtgttac cttaactaaa ttagatgggtg atacacgtgg tgggtgcagct 780
 41 ttatctattc gttcgggtgac acaaaaacca attaaatttg ttggtatgag tgaaaagtta 840
 42 gatggtttag agctattcca tcctgaacgt atggcatcac gtatttttagg tatgggtgat 900
 43 gtgttaagtt taattgaaaa agcgcaacaa gatgtggatc aagaaaaagc aaaagattta 960
 44 gagaaaaaga tgcgtgagtc atcgtttact ttagatgatt ttttagaaca acttgatcag 1020
 45 gtgaaaaatc taggaccact ggatgatatt atgaaaatga ttccagggtat gaataaaatg 1080
 46 aaagggctag ataagcttaa tatgagtga aagcaaattg atcatattaa agcgattatc 1140
 47 cagtcaatga cgccggctga aagaaacaat ccagacacat tgaatgtatc acgtaaaaag 1200
 48 cgtattgcta aagggtctgg tcgttcatta caagaagtca atcgtttgat gaaacaattt 1260
 49 aacgatatga agaaaatgat gaaacaattc actggtggcg gtaaaggtaa aaaaggtaaa 1320
 50 cgcaatcaaa tgcaaaatat gttaaaagggt atgaattttac cgttttaa 1368
 52 <210> SEQ ID NO: 2
 53 <211> LENGTH: 455
 54 <212> TYPE: PRT
 55 <213> ORGANISM: Staphylococcus aureus
 57 <400> SEQUENCE: 2
 58 Met Ala Phe Glu Gly Leu Ser Glu Arg Leu Gln Ala Thr Met Gln Lys
 59 1 5 10 15
 60 Met Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Lys Ile Met Met
 61 20 25 30

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62 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
63           35                     40                     45
64 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
65           50                     55                     60
66 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
67 65           70                     75                     80
68 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
69           85                     90                     95
70 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
71           100                    105                    110
72 Gly Lys Thr Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
73           115                    120                    125
74 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
75           130                    135                    140
76 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
77 145           150                    155                    160
78 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
79           165                    170                    175
80 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
81           180                    185                    190
82 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
83           195                    200                    205
84 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
85           210                    215                    220
86 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
87 225           230                    235                    240
88 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
89           245                    250                    255
90 Gly Gly Ala Ala Leu Ser Ile Arg Ser Val Thr Gln Lys Pro Ile Lys
91           260                    265                    270
92 Phe Val Gly Met Ser Glu Lys Leu Asp Gly Leu Glu Leu Phe His Pro
93           275                    280                    285
94 Glu Arg Met Ala Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu
95           290                    295                    300
96 Ile Glu Lys Ala Gln Gln Asp Val Asp Gln Glu Lys Ala Lys Asp Leu
97 305           310                    315                    320
98 Glu Lys Lys Met Arg Glu Ser Ser Phe Thr Leu Asp Asp Phe Leu Glu
99           325                    330                    335
100 Gln Leu Asp Gln Val Lys Asn Leu Gly Pro Leu Asp Asp Ile Met Lys
101           340                    345                    350
102 Met Ile Pro Gly Met Asn Lys Met Lys Gly Leu Asp Lys Leu Asn Met
103           355                    360                    365
104 Ser Glu Lys Gln Ile Asp His Ile Lys Ala Ile Ile Gln Ser Met Thr
105           370                    375                    380
106 Pro Ala Glu Arg Asn Asn Pro Asp Thr Leu Asn Val Ser Arg Lys Lys
107 385           390                    395                    400
108 Arg Ile Ala Lys Gly Ser Gly Arg Ser Leu Gln Glu Val Asn Arg Leu
109           405                    410                    415
110 Met Lys Gln Phe Asn Asp Met Lys Lys Met Met Lys Gln Phe Thr Gly

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```

111          420          425          430
112 Gly Gly Lys Gly Lys Lys Gly Lys Arg Asn Gln Met Gln Asn Met Leu
113          435          440          445
114 Lys Gly Met Asn Leu Pro Phe
115          450          455
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 792
119 <212> TYPE: DNA
120 <213> ORGANISM: Staphylococcus aureus
122 <400> SEQUENCE: 3
123 atggcatttg aaggtttatc agaacgcctg caagcgacga tgcaaaaaat gcgtggtaag      60
124 ggtaaaactta ctgaagctga tataaagata atgatgcgtg aagtaagatt agcgttatatt      120
125 gaggtctgacg taaacttttaa agtggtaaaa gaatttatta aaacagtatc agaacgcgca      180
126 ttaggttccg atgtaatgca atcattaaca ccaggggcaac aagttattaa aatagttcaa      240
127 gatgaattaa cgaagttgat ggggtggagaa aatacatcga ttaatatgtc aaataaacca      300
128 cctactgttg ttatgatggt tggttttacaa ggtgctggta aaacaacaac tgcaggtaaa      360
129 ttagcattat tgatgcgtaa aaaatacaac aaaaaaccta tgttagttgc agcagatatt      420
130 tatcgtccag cagcgataaa tcaattacaa acagtaggga aacaaattga tattcctgta      480
131 tacagtgaag gagatcaagt aaagccacaa caaattgtaa ctaatgcatt aaaacatgct      540
132 aaagaagaac atttagactt tgtaatcatt gatacagcag gtcgattaca catcgatgaa      600
133 gcattgatga acgaattaaa agaagtaaaa gaaattgcta aaccaaacga aattatgtta      660
134 gttgtcgatt caatgacggg tcaagatgct gtcaatgttg cagaatcttt tgacgatcaa      720
135 cttgatgtca cagggtgttac cttaactaaa ttagatggtg ataccctggt tgggtgcagct      780
136 ttatctattc gt                                     792
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 264
140 <212> TYPE: PRT
141 <213> ORGANISM: Staphylococcus aureus
143 <400> SEQUENCE: 4
144 Met Ala Phe Glu Gly Leu Ser Glu Arg Leu Gln Ala Thr Met Gln Lys
145 1          5          10          15
146 Met Arg Gly Lys Gly Lys Leu Thr Glu Ala Asp Ile Lys Ile Met Met
147          20          25          30
148 Arg Glu Val Arg Leu Ala Leu Phe Glu Ala Asp Val Asn Phe Lys Val
149          35          40          45
150 Val Lys Glu Phe Ile Lys Thr Val Ser Glu Arg Ala Leu Gly Ser Asp
151          50          55          60
152 Val Met Gln Ser Leu Thr Pro Gly Gln Gln Val Ile Lys Ile Val Gln
153          65          70          75          80
154 Asp Glu Leu Thr Lys Leu Met Gly Gly Glu Asn Thr Ser Ile Asn Met
155          85          90          95
156 Ser Asn Lys Pro Pro Thr Val Val Met Met Val Gly Leu Gln Gly Ala
157          100          105          110
158 Gly Lys Thr Thr Thr Ala Gly Lys Leu Ala Leu Leu Met Arg Lys Lys
159          115          120          125
160 Tyr Asn Lys Lys Pro Met Leu Val Ala Ala Asp Ile Tyr Arg Pro Ala
161          130          135          140
162 Ala Ile Asn Gln Leu Gln Thr Val Gly Lys Gln Ile Asp Ile Pro Val
163          145          150          155          160

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164 Tyr Ser Glu Gly Asp Gln Val Lys Pro Gln Gln Ile Val Thr Asn Ala
165                               165                               170                               175
166 Leu Lys His Ala Lys Glu Glu His Leu Asp Phe Val Ile Ile Asp Thr
167                               180                               185                               190
168 Ala Gly Arg Leu His Ile Asp Glu Ala Leu Met Asn Glu Leu Lys Glu
169                               195                               200                               205
170 Val Lys Glu Ile Ala Lys Pro Asn Glu Ile Met Leu Val Val Asp Ser
171                               210                               215                               220
172 Met Thr Gly Gln Asp Ala Val Asn Val Ala Glu Ser Phe Asp Asp Gln
173 225                               230                               235                               240
174 Leu Asp Val Thr Gly Val Thr Leu Thr Lys Leu Asp Gly Asp Thr Arg
175                               245                               250                               255
176 Gly Gly Ala Ala Leu Ser Ile Arg
177                               260
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 500
181 <212> TYPE: DNA
182 <213> ORGANISM: Staphylococcus aureus
184 <400> SEQUENCE: 5
185 aaacatcttg caaatgaatt taaatttaac gacttctcaa gacgtcgtat aaagtaaaca      60
186 atgatataaa tgatttatac ttgcaattaa ctattaaaat atagtaatat atatcttgcc      120
187 gtgctaggtg gggaggtagc ggttcctgt actcgaaatc cgctttatgc gaggcttaat      180
188 tcctttgttg aggccgtatt tttgcgaagt ctgcccagaag cacgtagtgt ttgaagattt      240
189 cggtcctatg caatatgaac ccatgaacca tgtcagggtc tgacggaagc agcattaagt      300
190 ggatcatcat atgtgccgta gggtagccga gatttagcta acgactttgg ttacgttcgt      360
191 gaattacgtt cgatgcttag gtgcacgggt ttttattttt taaatattaa accgattatt      420
192 aagagttgaa aatatatatt tatttataga agctactttc ttgaagacaa ttcagcgtat      480
193 tatacgtgga acatgtttgt
194                               500
195 <210> SEQ ID NO: 6
196 <211> LENGTH: 358
197 <212> TYPE: DNA
198 <213> ORGANISM: Staphylococcus aureus
200 <400> SEQUENCE: 6
201 acttgcaatt aactattaaa atatagtaat atatatcttg ccgtgctagg tggggaggta      60
202 gcggttccct gtactcgaaa tccgctttat gcgaggctta attcctttgt tgaggccgta      120
203 tttttgcgaa gtctgcccaa agcacgtagt gtttgaagat ttcggtccta tgcaatatga      180
204 acccatgaac catgtcaggc cctgacggaa gcagcattaa gtggatcatc atatgtgccg      240
205 tagggtagcc gagatttagc taacgacttt ggttacgttc gtgaattacg ttcgatgctt      300
206 aggtgcacgg ttttttattt tttaaatatt aaaccgatta ttaagagttg aaaatata      358
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 276
210 <212> TYPE: DNA
211 <213> ORGANISM: Staphylococcus aureus
213 <400> SEQUENCE: 7
214 cttgccgtgc taggtgggga ggtagcgggt ccctgtactc gaaatccgct ttatgcgagg      60
215 cttaattcct ttgttgaggc cgtatttttg cgaagtctgc ccaaagcacg tagtgtttga      120
216 agatttcggt cctatgcaat atgaacccat gaaccatgtc aggtcctgac ggaagcagca      180
217 ttaagtggat catcatatgt gccgtagggt agccgagatt tagctaacga ctttggttac      240
218 gttcgtgaat tacgttcgat gcttaggtgc acggtt
219                               276

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220 <210> SEQ ID NO: 8
221 <211> LENGTH: 275
222 <212> TYPE: DNA
223 <213> ORGANISM: Staphylococcus aureus
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: (1)...(275)
228 <223> OTHER INFORMATION: n = A,T,C or G
230 <400> SEQUENCE: 8
231 aacaatgccg ttccaatata atatttcaaa acatcttgca aatgaattta aatttaccga      60
232 cttctcaaga cgtcgtataa agtaaacaat gatataaatg atttatactt gcaattaact      120
W--> 233 attnaaatat agtaatatat atctttccgt gctaggtggg gaggtagcgg ttccctgtac      180
234 tcgaaatccg ctttatgcga ggcttaattc ctttgttgag gccgtatttt tgogaagtct      240
235 gcccaaagca cgtagtgttt gaagatttcg gtcct                                275

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/943,108

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TIME: 12:19:41

Input Set : N:\Crf3\RULE60\09943108.txt

Output Set: N:\CRF3\09262001\I943108.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8